

# METHOD FOR THE PREDICTION OF BINDING TARGETS AND THE DESIGN OF LIGANDS

## ABSTRACT

A computer-based method for the identification of binding targets in proteins  
5 and other macromolecules. More particularly, the invention includes an algorithm  
aimed at predicting binding targets in proteins. This algorithm, named Woolford,  
requires knowledge of the high resolution structure of the protein but no knowledge of  
the location or identity of natural binding sites or ligands. Binding targets in the  
protein are identified and classified according to their expected optimal affinities.

10 Binding targets can be located at the protein surface or at internal surfaces that become  
exposed as a result of partial unfolding, conformational changes, subunit dissociation,  
or other events. The entire protein is mapped according to the binding potential of its  
constituent atoms. Once binding targets are identified, optimal ligands are designed and  
progressively built by the addition of individual atoms that complement structurally  
15 and energetically the selected target. This algorithm is expected to have significant  
applications in structure-based drug design since it allows: 1) identification of binding  
targets in proteins; 2) identification of additional targets if the primary target is known;  
3) design of ligand molecules with optimal binding affinities for the selected target;  
and 4) refinement of lead compounds by defining the location and nature of chemical  
20 groups for optimal binding affinity.

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